

Ryan A Flynn

List of Publications by Year in descending order

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57
papers

16,974
citations

66234

42
h-index

128067

60
g-index

71
all docs

71
docs citations

71
times ranked

25420
citing authors

#	ARTICLE	IF	CITATIONS
1	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011, 470, 279-283.	13.7	1,949
2	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011, 472, 120-124.	13.7	1,760
3	c-Myc Regulates Transcriptional Pause Release. <i>Cell</i> , 2010, 141, 432-445.	13.5	1,104
4	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 707-719.	5.2	990
5	Systematic Discovery of Xist RNA Binding Proteins. <i>Cell</i> , 2015, 161, 404-416.	13.5	886
6	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016, 13, 919-922.	9.0	853
7	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	13.7	810
8	Divergent Transcription from Active Promoters. <i>Science</i> , 2008, 322, 1849-1851.	6.0	801
9	Structural imprints in vivo decode RNA regulatory mechanisms. <i>Nature</i> , 2015, 519, 486-490.	13.7	639
10	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016, 165, 1267-1279.	13.5	520
11	Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , 2014, 505, 706-709.	13.7	519
12	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015, 522, 221-225.	13.7	507
13	Long Noncoding RNAs in Cell-Fate Programming and Reprogramming. <i>Cell Stem Cell</i> , 2014, 14, 752-761.	5.2	461
14	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	9.4	419
15	RNA SHAPE analysis in living cells. <i>Nature Chemical Biology</i> , 2013, 9, 18-20.	3.9	366
16	Quantitative analysis of EGFRvIII cellular signaling networks reveals a combinatorial therapeutic strategy for glioblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12867-12872.	3.3	365
17	The Mammalian Ribo-interactome Reveals Ribosome Functional Diversity and Heterogeneity. <i>Cell</i> , 2017, 169, 1051-1065.e18.	13.5	314
18	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020, 588, 670-675.	13.7	273

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19	Small RNAs are modified with N-glycans and displayed on the surface of living cells. <i>Cell</i> , 2021, 184, 3109-3124.e22.	13.5	260
20	RNA helicase DDX21 coordinates transcription and ribosomal RNA processing. <i>Nature</i> , 2015, 518, 249-253.	13.7	232
21	irCLIP platform for efficient characterization of protein-RNA interactions. <i>Nature Methods</i> , 2016, 13, 489-492.	9.0	222
22	Transcriptional profiling of long non-coding RNAs and novel transcribed regions across a diverse panel of archived human cancers. <i>Genome Biology</i> , 2012, 13, R75.	13.9	221
23	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	9.4	195
24	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. <i>Cell Stem Cell</i> , 2015, 17, 675-688.	5.2	177
25	Essential role of lncRNA binding for WDR5 maintenance of active chromatin and embryonic stem cell pluripotency. <i>ELife</i> , 2014, 3, e02046.	2.8	176
26	Antisense RNA polymerase II divergent transcripts are P-TEFb dependent and substrates for the RNA exosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10460-10465.	3.3	167
27	DDX5 and its associated lncRNA Rmp modulate TH17 cell effector functions. <i>Nature</i> , 2015, 528, 517-522.	13.7	154
28	Transcriptome-wide interrogation of RNA secondary structure in living cells with icSHAPE. <i>Nature Protocols</i> , 2016, 11, 273-290.	5.5	147
29	Inhibition of NGLY1 Inactivates the Transcription Factor Nrf1 and Potentiates Proteasome Inhibitor Cytotoxicity. <i>ACS Central Science</i> , 2017, 3, 1143-1155.	5.3	146
30	Discovery and functional interrogation of SARS-CoV-2 RNA-host protein interactions. <i>Cell</i> , 2021, 184, 2394-2411.e16.	13.5	141
31	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. <i>Nature</i> , 2018, 554, 112-117.	13.7	125
32	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 231-238.	3.6	92
33	An RNA-centric dissection of host complexes controlling flavivirus infection. <i>Nature Microbiology</i> , 2019, 4, 2369-2382.	5.9	79
34	Dissecting noncoding and pathogen RNA-protein interactomes. <i>Rna</i> , 2015, 21, 135-143.	1.6	71
35	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016, 62, 34-46.	4.5	71
36	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019, 16, 489-492.	9.0	70

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37	Comparison of SHAPE reagents for mapping RNA structures inside living cells. <i>Rna</i> , 2017, 23, 169-174.	1.6	62
38	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	0.8	62
39	The novel lncRNA lnc-NR2F1 is pro-neurogenic and mutated in human neurodevelopmental disorders. <i>ELife</i> , 2019, 8, .	2.8	59
40	DNA-PKcs has KU-dependent function in rRNA processing and haematopoiesis. <i>Nature</i> , 2020, 579, 291-296.	13.7	57
41	<scp>RNA</scp> structural analysis by evolving <scp>SHAPE</scp> chemistry. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014, 5, 867-881.	3.2	54
42	Active chromatin and noncoding RNAs: an intimate relationship. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 172-178.	1.5	45
43	Diagnosis, Treatment, and Management of Breast Cancer in Previously Augmented Women. <i>Breast Journal</i> , 2006, 12, 343-348.	0.4	43
44	Phosphotyrosine signaling analysis of site-specific mutations on EGFRvIII identifies determinants governing glioblastoma cell growth. <i>Molecular BioSystems</i> , 2010, 6, 1227.	2.9	40
45	RNA helicase DDX21 mediates nucleotide stress responses in neural crest and melanoma cells. <i>Nature Cell Biology</i> , 2020, 22, 372-379.	4.6	37
46	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019, 10, 5712.	5.8	27
47	Proteomic analysis of young and old mouse hematopoietic stem cells and their progenitors reveals post-transcriptional regulation in stem cells. <i>ELife</i> , 2020, 9, .	2.8	21
48	Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-Protein Interfaces. <i>Molecular Cell</i> , 2020, 80, 903-914.e8.	4.5	20
49	The CD22-IGF2R interaction is a therapeutic target for microglial lysosome dysfunction in Niemann-Pick type C. <i>Science Translational Medicine</i> , 2021, 13, eabg2919.	5.8	18
50	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0165913.	1.1	11
51	An atlas of posttranslational modifications on RNA binding proteins. <i>Nucleic Acids Research</i> , 2022, 50, 4329-4339.	6.5	8
52	Comparative Analysis Reveals Furoyl <i>in Vivo</i> Selective Hydroxyl Acylation Analyzed by Primer Extension Reagents Form Stable Ribosyl Ester Adducts. <i>Biochemistry</i> , 2017, 56, 1811-1814.	1.2	6
53	Diverse functional elements in RNA predicted transcriptome-wide by orthogonal RNA structure probing. <i>Nucleic Acids Research</i> , 2021, 49, 11868-11882.	6.5	5
54	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, 7279-7297.	6.5	4

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55	Loquacious modulates flaviviral RNA replication in mosquito cells. PLoS Pathogens, 2022, 18, e1010163.	2.1	3
56	fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. STAR Protocols, 2021, 2, 100762.	0.5	1
57	HiChIRP: RNA-centric chromatin conformation. Protocol Exchange, 0, , .	0.3	1